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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/581,894A

DATE: 04/18/2002

TIME: 14:56:22

Input Set : A:\20146P - SeqList.txt

Output Set: N:\CRF3\04182002\I581894A.raw

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4 <110> APPLICANT: Fong, Tung Ming
5     van der Ploeg, Leonardus H. T.
6     Tota, Michael R.
8 <120> TITLE OF INVENTION: C-TERMINAL REGION OF AGOUTI-RELATED
9     TRANSCRIPT (ART) PROTEIN
11 <130> FILE REFERENCE: 20146P
13 <140> CURRENT APPLICATION NUMBER: 09/581,894A
14 <141> CURRENT FILING DATE: 2000-08-21
16 <150> PRIOR APPLICATION NUMBER: PCT/US98/26457
17 <151> PRIOR FILING DATE: 1998-12-11
19 <150> PRIOR APPLICATION NUMBER: 60/069,747
20 <151> PRIOR FILING DATE: 1997-12-16
22 <160> NUMBER OF SEQ ID NOS: 24
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 118
28 <212> TYPE: PRT
29 <213> ORGANISM: Human
31 <400> SEQUENCE: 1
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33 1             5             10             15
34 Leu Glu His Thr His Arg Arg Gly Ser Leu Val Lys Arg Ser Ser Leu
35             20             25             30
36 Gln Asp Arg Glu Pro Arg Ser Ser Arg Arg Cys Val Arg Leu His Glu
37             35             40             45
38 Ser Cys Leu Gly Gln Gln Val Pro Cys Cys Asp Pro Cys Ala Thr Cys
39             50             55             60
40 Tyr Cys Arg Phe Phe Asn Ala Phe Cys Tyr Cys Arg Lys Leu Gly Thr
41 65             70             75             80
42 Ala Met Asn Pro Cys Ser Arg Thr Leu Val Pro Arg Gly Ser Glu Gln
43             85             90             95
44 Lys Leu Ile Ser Glu Glu Asp Leu Asn Leu Arg Arg Ala Ser Leu Gly
45             100            105            110
46 His His His His His His
47             115
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 120
51 <212> TYPE: PRT
52 <213> ORGANISM: Human
54 <400> SEQUENCE: 2
55 Met Leu Thr Ala Ala Leu Leu Ser Cys Ala Leu Leu Leu Ala Leu Pro
56 1             5             10             15
57 Ala Thr Arg Gly Ala Gln Met Gly Leu Ala Leu Gln Asp Arg Glu Pro

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58          20          25          30
59 Arg Ser Ser Arg Arg Cys Val Arg Leu His Glu Ser Cys Leu Gly Gln
60          35          40          45
61 Gln Val Pro Cys Cys Asp Pro Cys Ala Thr Cys Tyr Cys Arg Phe Phe
62          50          55          60
63 Asn Ala Phe Cys Tyr Cys Arg Lys Leu Gly Thr Ala Met Asn Pro Cys
64 65          70          75          80
65 Ser Arg Thr Leu Val Pro Arg Gly Ser Gly Ser Glu Leu Gly Thr Lys
66          85          90          95
67 Leu Gly Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala
68          100          105          110
69 Val Asp His His His His His His
70          115          120
72 <210> SEQ ID NO: 3
73 <211> LENGTH: 121
74 <212> TYPE: PRT
75 <213> ORGANISM: Human
77 <400> SEQUENCE: 3
78 Met Leu Thr Ala Ala Leu Leu Ser Cys Ala Leu Leu Leu Ala Leu Pro
79 1          5          10          15
80 Ala Thr Arg Gly Ala Gln Met Gly Leu Ala Leu Gln Asp Arg Glu Pro
81          20          25          30
82 Arg Ser Ser Arg Arg Cys Val Arg Leu His Glu Ser Cys Leu Gly Gln
83          35          40          45
84 Gln Val Pro Cys Cys Asp Pro Cys Ala Thr Cys Tyr Cys Arg Phe Phe
85          50          55          60
86 Asn Ala Phe Cys Tyr Cys Arg Lys Leu Gly Thr Ala Met Asn Pro Cys
87 65          70          75          80
88 Ser Arg Thr Leu Val Pro Arg Gly Ser Gly Ser Leu Arg Arg Ala Ser
89          85          90          95
90 Leu Gly Lys Leu Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser
91          100          105          110
92 Ala Val Asp His His His His His His
93          115          120
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 654
97 <212> TYPE: PRT
98 <213> ORGANISM: Human
100 <400> SEQUENCE: 4
101 Met Leu Thr Ala Ala Leu Leu Ser Cys Ala Leu Leu Leu Ala Leu Pro
102 1          5          10          15
103 Ala Thr Arg Gly Ala Gln Met Gly Leu Ala Pro Met Glu Gly Ile Arg
104          20          25          30
105 Arg Pro Asp Gln Ala Leu Leu Pro Glu Leu Pro Gly Leu Gly Leu Arg
106          35          40          45
107 Ala Pro Leu Lys Lys Thr Asn Ala Glu Gln Ala Glu Glu Asp Leu Leu
108          50          55          60
109 Gln Glu Ala Gln Ala Leu Ala Glu Val Leu Asp Leu Gln Asp Arg Glu
110 65          70          75          80

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111 Pro Arg Ser Ser Arg Arg Cys Val Arg Leu His Glu Ser Cys Leu Gly
112                               85                               90                               95
113 Gln Gln Val Pro Cys Cys Asp Pro Cys Ala Thr Cys Tyr Cys Arg Phe
114                               100                               105                               110
115 Phe Asn Ala Phe Cys Tyr Cys Arg Lys Leu Gly Thr Ala Met Asn Pro
116                               115                               120                               125
117 Cys Ser Arg Thr Leu Val Pro Arg Gly Ser Gly Ser Ile Ile Pro Val
118                               130                               135                               140
119 Glu Glu Glu Asn Pro Asp Phe Trp Asn Arg Gln Ala Ala Glu Ala Leu
120 145                               150                               155                               160
121 Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr Ala Ala Lys Asn Leu
122                               165                               170                               175
123 Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser Thr Val Thr Ala Ala
124                               180                               185                               190
125 Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu Gly Pro Glu Thr Phe
126                               195                               200                               205
127 Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu Ser Lys Thr Tyr Ser
128                               210                               215                               220
129 Val Asp Lys His Val Pro Asp Ser Gly Ala Thr Ala Thr Ala Tyr Leu
130 225                               230                               235                               240
131 Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly Leu Ser Ala Ala Ala
132                               245                               250                               255
133 Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn Glu Val Ile Ser Val
134                               260                               265                               270
135 Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val Gly Val Val Thr Thr
136                               275                               280                               285
137 Thr Arg Val Gln His Ala Ser Pro Ala Gly Ala Tyr Ala His Thr Val
138                               290                               295                               300
139 Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro Ala Ser Ala Arg Gln
140 305                               310                               315                               320
141 Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile Ser Asn Met Asp Ile
142                               325                               330                               335
143 Asp Val Ile Leu Gly Gly Gly Arg Lys Tyr Met Phe Pro Met Gly Thr
144                               340                               345                               350
145 Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln Gly Gly Thr Arg Leu
146                               355                               360                               365
147 Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala Lys His Gln Gly Ala
148                               370                               375                               380
149 Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln Ala Ser Leu Asp Pro
150 385                               390                               395                               400
151 Ser Val Thr His Leu Met Gly Leu Phe Glu Pro Gly Asp Met Lys Tyr
152                               405                               410                               415
153 Glu Ile His Arg Asp Ser Thr Leu Asp Pro Ser Leu Met Glu Met Thr
154                               420                               425                               430
155 Glu Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro Arg Gly Phe Phe Leu
156                               435                               440                               445
157 Phe Val Glu Gly Gly Arg Ile Asp His Gly His His Glu Ser Arg Ala
158                               450                               455                               460
159 Tyr Arg Ala Leu Thr Glu Thr Ile Met Phe Asp Asp Ala Ile Glu Arg

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160 465          470          475          480
161 Ala Gly Gln Leu Thr Ser Glu Glu Asp Thr Leu Ser Leu Val Thr Ala
162          485          490          495
163 Asp His Ser His Val Phe Ser Phe Gly Gly Tyr Pro Leu Arg Gly Ser
164          500          505          510
165 Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Arg Asp Arg Lys Ala Tyr
166          515          520          525
167 Thr Val Leu Leu Tyr Gly Asn Gly Pro Gly Tyr Val Leu Lys Asp Gly
168          530          535          540
169 Ala Arg Pro Asp Val Thr Glu Ser Glu Ser Gly Ser Pro Glu Tyr Arg
170 545          550          555          560
171 Gln Gln Ser Ala Val Pro Leu Asp Gly Glu Thr His Ala Gly Glu Asp
172          565          570          575
173 Val Ala Val Phe Ala Arg Gly Pro Gln Ala His Leu Val His Gly Val
174          580          585          590
175 Gln Glu Gln Thr Phe Ile Ala His Val Met Ala Phe Ala Ala Cys Leu
176          595          600          605
177 Glu Pro Tyr Thr Ala Cys Asp Leu Ala Pro Ser Ala Gly Thr Thr Asp
178          610          615          620
179 Ala Ala His Pro Gly Lys Leu Gly Pro Glu Gln Lys Leu Ile Ser Glu
180 625          630          635          640
181 Glu Asp Leu Asn Ser Ala Val Asp His His His His His
182          645          650
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 715
186 <212> TYPE: PRT
187 <213> ORGANISM: Human
189 <400> SEQUENCE: 5
190 Met Leu Thr Ala Ala Leu Leu Ser Cys Ala Leu Leu Leu Ala Leu Pro
191 1          5          10          15
192 Ala Thr Arg Gly Ala Gln Met Gly Leu Ala Pro Met Glu Gly Ile Arg
193          20          25          30
194 Arg Pro Asp Gln Ala Leu Leu Pro Glu Leu Pro Gly Leu Gly Leu Arg
195          35          40          45
196 Ala Pro Leu Lys Lys Thr Asn Ala Glu Gln Ala Glu Glu Asp Leu Leu
197          50          55          60
198 Gln Glu Ala Gln Ala Leu Ala Glu Val Leu Asp Leu Gln Asp Arg Glu
199 65          70          75          80
200 Pro Arg Ser Ser Arg Arg Cys Val Arg Leu His Glu Ser Cys Leu Gly
201          85          90          95
202 Gln Gln Val Pro Cys Cys Asp Pro Cys Ala Thr Cys Tyr Cys Arg Phe
203          100          105          110
204 Phe Asn Ala Phe Cys Tyr Cys Arg Lys Leu Gly Thr Ala Met Asn Pro
205          115          120          125
206 Cys Ser Arg Thr Leu Val Pro Arg Gly Ser Gly Ser Met Ser Ile Glu
207          130          135          140
208 Asn Asn Ile Leu Ile Gly Pro Pro Pro Tyr Tyr Pro Leu Glu Glu Gly
209 145          150          155          160
210 Thr Ala Gly Glu Gln Leu His Arg Ala Ile Ser Arg Tyr Ala Ala Val

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211          165          170          175
212 Pro Gly Thr Leu Ala Tyr Thr Asp Val His Thr Glu Leu Glu Val Thr
213          180          185          190
214 Tyr Lys Glu Phe Leu Asp Val Thr Cys Arg Leu Ala Glu Ala Met Lys
215          195          200          205
216 Asn Tyr Gly Leu Gly Leu Gln His Thr Ile Ser Val Cys Ser Glu Asn
217          210          215          220
218 Cys Val Gln Phe Phe Met Pro Ile Cys Ala Ala Leu Tyr Val Gly Val
219 225          230          235          240
220 Ala Thr Ala Pro Thr Asn Asp Ile Tyr Asn Glu Arg Glu Leu Tyr Asn
221          245          250          255
222 Ser Leu Ser Ile Ser Gln Pro Thr Val Val Phe Thr Ser Arg Asn Ser
223          260          265          270
224 Leu Gln Lys Ile Leu Gly Val Gln Ser Arg Leu Pro Ile Ile Lys Lys
225          275          280          285
226 Ile Ile Ile Leu Asp Gly Lys Lys Asp Tyr Leu Gly Tyr Gln Ser Met
227          290          295          300
228 Gln Ser Phe Met Lys Glu His Val Pro Ala Asn Phe Asn Val Ser Ala
229 305          310          315          320
230 Phe Lys Pro Leu Ser Phe Asp Leu Asp Arg Val Ala Cys Ile Met Asn
231          325          330          335
232 Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val Pro Ile Ser His Arg
233          340          345          350
234 Asn Thr Ile Tyr Arg Phe Ser His Cys Arg Asp Pro Val Phe Gly Asn
235          355          360          365
236 Gln Ile Ile Pro Asp Thr Thr Ile Leu Cys Ala Val Pro Phe His His
237          370          375          380
238 Ala Phe Gly Thr Phe Thr Asn Leu Gly Tyr Leu Ile Cys Gly Phe His
239 385          390          395          400
240 Val Val Leu Met Tyr Arg Phe Asn Glu His Leu Phe Leu Gln Thr Leu
241          405          410          415
242 Gln Asp Tyr Lys Cys Gln Ser Ala Leu Leu Val Pro Thr Val Leu Ala
243          420          425          430
244 Phe Leu Ala Lys Asn Pro Leu Val Asp Lys Tyr Asp Leu Ser Asn Leu
245          435          440          445
246 His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys Glu Ile Ser Glu
247          450          455          460
248 Ile Ala Ala Lys Arg Phe Lys Leu Pro Gly Ile Arg Gln Gly Tyr Gly
249 465          470          475          480
250 Leu Thr Glu Thr Thr Cys Ala Ile Val Ile Thr Ala Glu Gly Glu Phe
251          485          490          495
252 Lys Leu Gly Ala Val Gly Lys Val Val Pro Phe Tyr Ser Leu Lys Val
253          500          505          510
254 Leu Asp Leu Asn Thr Gly Lys Lys Leu Gly Pro Asn Glu Arg Gly Glu
255          515          520          525
256 Ile Cys Phe Lys Gly Pro Met Ile Met Lys Gly Tyr Ile Asn Asn Pro
257          530          535          540
258 Glu Ala Thr Arg Glu Leu Ile Asp Glu Glu Gly Trp Ile His Ser Gly
259 545          550          555          560

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VERIFICATION SUMMARY

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